

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
 BINDING DOMAINS FOR CELL-SPECIFIC TARGETING

<130> 9237.21WO

<160> 27

<170> PatentIn version 3.2

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Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr	
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Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
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Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
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Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
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Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu

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gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt gca 192
 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
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 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 35 40 45
 aag aag gac aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat 192
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 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
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 aca ttt gaa gaa gca aca gca gaa gca tac aga tat gct gac tta tta 144
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45
 gca aaa gaa aat ggt aaa tat aca gta gac gtt gca gat aaa ggt tat 192
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aca ttt gca gaa gca aca gca gaa gca tac aga tac gct gac tta tta 144
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Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu
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Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu
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 Ser Tyr Cys His His Thr Glu Pro Cys Phe Ser Pro Val Lys Ile Glu
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 Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser
 35 40 45
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 Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr
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Pro	Asp	Leu	Ile	Arg	His	Asp	Asp	His	Thr	Ala	Gln	Gly	Lys	Leu	His	245	250	255	
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His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile
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Thr Ala Met Cys Leu Leu Gly Asn Val Ser Phe Pro Cys Asp Arg Pro	
10 15 20	
ccc aca tgc tat acc cgc gaa cct tcc aga gcc ctc gac atc ctt gaa	8552
Pro Thr Cys Tyr Thr Arg Glu Pro Ser Arg Ala Leu Asp Ile Leu Glu	
25 30 35	
gag aac gtg aac cat gag gcc tac gat acc ctg ctc aat gcc ata ttg	8600
Glu Asn Val Asn His Glu Ala Tyr Asp Thr Leu Leu Asn Ala Ile Leu	
40 45 50	
cgg tgc gga tcg tct ggc aga agc aaa aga agc gtc att gac gac ttt	8648
Arg Cys Gly Ser Ser Gly Arg Ser Lys Arg Ser Val Ile Asp Asp Phe	
55 60 65 70	
acc ctg acc agc ccc tac ttg ggc aca tgc tcg tac tgc cac cat act	8696
Thr Leu Thr Ser Pro Tyr Leu Gly Thr Cys Ser Tyr Cys His His Thr	
75 80 85	
gta ccg tgc ttc agc cct gtt aag atc gag cag gtc tgg gac gaa gcg	8744
Val Pro Cys Phe Ser Pro Val Lys Ile Glu Gln Val Trp Asp Glu Ala	
90 95 100	
gac gat aac acc ata cgc ata cag act tcc gcc cag ttt gga tac gac	8792
Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser Ala Gln Phe Gly Tyr Asp	
105 110 115	
caa agc gga gca gca agc gca aac aag tac cgc tac atg tcg ctt aag	8840
Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr Arg Tyr Met Ser Leu Lys	
120 125 130	
cag gat cac acc gtt aaa gaa ggc acc atg gat gac atc aag att agc	8888
Gln Asp His Thr Val Lys Glu Gly Thr Met Asp Asp Ile Lys Ile Ser	
135 140 145 150	
acc tca gga ccg tgt aga agg ctt agc tac aaa gga tac ttt ctc ctc	8936
Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr Lys Gly Tyr Phe Leu Leu	
155 160 165	
gca aaa tgc cct cca ggg gac agc gta acg gtt agc ata gtg agt agc	8984
Ala Lys Cys Pro Pro Gly Asp Ser Val Thr Val Ser Ile Val Ser Ser	
170 175 180	
aac tca gca acg tca tgt aca ctg gcc cgc aag ata aaa cca aaa ttc	9032
Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg Lys Ile Lys Pro Lys Phe	
185 190 195	
gtg gga cgg gaa aaa tat gat cta cct ccc gtt cac ggt aaa aaa att	9080
Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro Val His Gly Lys Lys Ile	
200 205 210	
cct tgc aca gtg tac gac cgt ctg aaa gaa aca act gca ggc tac atc	9128
Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu Thr Thr Ala Gly Tyr Ile	
215 220 225 230	

act	atg	cac	agg	ccg	aga	ccg	cac	gct	tat	aca	tcc	tac	ctg	gaa	gaa	9176
Thr	Met	His	Arg	Pro	Arg	Pro	His	Ala	Tyr	Thr	Ser	Tyr	Leu	Glu	Glu	
				235				240						245		
tca	tca	ggg	aaa	gtt	tac	gca	aag	ccg	cca	tct	ggg	aag	aac	att	acg	9224
Ser	Ser	Gly	Lys	Val	Tyr	Ala	Lys	Pro	Pro	Ser	Gly	Lys	Asn	Ile	Thr	
			250					255					260			
tat	gag	tgc	aag	tgc	ggc	gac	tac	aag	acc	gga	acc	gtt	tcg	acc	cgc	9272
Tyr	Glu	Cys	Lys	Cys	Gly	Asp	Tyr	Lys	Thr	Gly	Thr	Val	Ser	Thr	Arg	
		265					270					275				
acc	gaa	atc	act	ggc	tgc	acc	gcc	atc	aag	cag	tgc	gtc	gcc	tat	aag	9320
Thr	Glu	Ile	Thr	Gly	Cys	Thr	Ala	Ile	Lys	Gln	Cys	Val	Ala	Tyr	Lys	
	280					285				290						
agc	gac	caa	acg	aag	tgg	gtc	ttc	aac	tca	ccg	gac	ttg	atc	aga	cat	9368
Ser	Asp	Gln	Thr	Lys	Trp	Val	Phe	Asn	Ser	Pro	Asp	Leu	Ile	Arg	His	
295					300					305					310	
gac	gac	cac	acg	gcc	caa	ggg	aaa	ttg	cat	ttg	cct	ttc	aag	ttg	atc	9416
Asp	Asp	His	Thr	Ala	Gln	Gly	Lys	Leu	His	Leu	Pro	Phe	Lys	Leu	Ile	
				315				320						325		
ccg	agt	acc	tgc	atg	gtc	cct	gtt	gcc	cac	gcg	ccg	aat	gta	ata	cat	9464
Pro	Ser	Thr	Cys	Met	Val	Pro	Val	Ala	His	Ala	Pro	Asn	Val	Ile	His	
			330					335					340			
ggc	ttt	aaa	cac	atc	agc	ctc	caa	tta	gat	aca	gac	cac	ttg	aca	ttg	9512
Gly	Phe	Lys	His	Ile	Ser	Leu	Gln	Leu	Asp	Thr	Asp	His	Leu	Thr	Leu	
		345					350					355				
ctc	acc	acc	agg	aga	cta	ggg	gca	aac	ccg	gaa	cca	acc	act	gaa	tgg	9560
Leu	Thr	Thr	Arg	Arg	Leu	Gly	Ala	Asn	Pro	Glu	Pro	Thr	Thr	Glu	Trp	
	360					365				370						
atc	gtc	gga	aag	acg	gtc	aga	aac	ttc	acc	gtc	gac	cga	gat	ggc	ctg	9608
Ile	Val	Gly	Lys	Thr	Val	Arg	Asn	Phe	Thr	Val	Asp	Arg	Asp	Gly	Leu	
375					380					385					390	
gaa	tac	ata	tgg	gga	aat	cat	gag	cca	gtg	agg	gtc	tat	gcc	caa	gag	9656
Glu	Tyr	Ile	Trp	Gly	Asn	His	Glu	Pro	Val	Arg	Val	Tyr	Ala	Gln	Glu	
			395					400						405		
tca	gca	cca	gga	gac	cct	cac	gga	tgg	cca	cac	gaa	ata	gta	cag	cat	9704
Ser	Ala	Pro	Gly	Asp	Pro	His	Gly	Trp	Pro	His	Glu	Ile	Val	Gln	His	
			410					415					420			
tac	tac	cat	cgc	cat	cct	gtg	tac	acc	atc	tta	gcc	gtc	gca	tca	gct	9752
Tyr	Tyr	His	Arg	His	Pro	Val	Tyr	Thr	Ile	Leu	Ala	Val	Ala	Ser	Ala	
		425					430					435				
acc	gtg	gcg	atg	atg	att	ggc	gta	act	gtt	gca	gtg	tta	tgt	gcc	tgt	9800
Thr	Val	Ala	Met	Met	Ile	Gly	Val	Thr	Val	Ala	Val	Leu	Cys	Ala	Cys	
	440					445					450					
aaa	gcg	cgc	cgt	gag	tgc	ctg	acg	cca	tac	gcc	ctg	gcc	cca	aac	gcc	9848

Lys	Ala	Arg	Arg	Glu	Cys	Leu	Thr	Pro	Tyr	Ala	Leu	Ala	Pro	Asn	Ala	
455					460					465					470	
gta atc cca act tcg ctg gca ctc ttg tgc tgc gtt agg tcg gcc aat 9896																
Val	Ile	Pro	Thr	Ser	Leu	Ala	Leu	Leu	Cys	Cys	Val	Arg	Ser	Ala	Asn	
				475					480					485		
gct gaaacgttca ccgagaccat gagttacttg tggtcgaaca gtcagccgtt 9949																
Ala																
cttctgggtc cagttgtgca tacctttggc cgctttcacc gttctaattgc gctgctgctc 10009																
ctgctgcctg ccttttttag tggttgccgg cgctacctg gcgaaggtag acgcctacga 10069																
acatgcgacc actgttccaa atgtgccaca gataccgtat aaggcacttg ttgaaagggc 10129																
agggatatgcc ccgctcaatt tggagatcac tgtcatgtcc tcggaggttt tgccttcacc 10189																
caaccaagag tacattacct gcaaattcac cactgtggtc ccctcccaa aaatcaaattg 10249																
ctgcggctcc ttggaatgtc agcgggccgc tcatgcagac tatacctgca aggtcttcgg 10309																
aggggtctac ccctttatgt ggggaggagc gcaatgtttt tgcgacagtg agaacagcca 10369																
gatgagtgag gcgtacgtcg aattgtcagc agattgcgcg tctgaccacg cgcaggcgat 10429																
taaggtgcac actgccgcga tgaaagtagg actgcgtatt gtgtacggga aactaccag 10489																
tttcctagat gtgtacgtga acggagtcac accaggaacg tctaaagact tgaaagtcac 10549																
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cattcaagct acctccttga ctagcaagga tctcatcgcc agcacagaca ttaggctact 10729																
caagccttcc gccagaacg tgcattgtccc gtacacgcag gcctcatcag gatttgagat 10789																
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agtaaattccg ctccgagcgg tggactgttc atacgggaac attcccattt ctattgacat 10909																
cccgaacgct gcctttatca ggacatcaga tgcaccactg gtctcaacag tcaaattgtga 10969																
agtcagttag tgcacttatt cagcagactt cggcgggatg gccaccctgc agtatgtatc 11029																
cgaccgcgaa ggtcaatgcc ccgtacattc gcattcgagc acagcaactc tccaagagtc 11089																
gacagtacat gtcctggaga aaggagcggg gacagtacac tttagcaccg cgagtccaca 11149																
ggcgaacttt atcgtatcgc tgtgtgggaa gaagacaaca tgcaatgcag aatgtaaacc 11209																
accagctgac catatcgtga gcaccccgca caaaaatgac caagaatttc aagccgccat 11269																
ctcaaaaaca tcatggagtt ggctgtttgc ccttttcggc ggcgcctcgt cgctattaat 11329																

tataggactt atgatttttg cttgcagcat gatgctgact agcacacgaa gatgaccgct 11389
 acgccccaat gatccgacca gcaaaactcg atgtacttcc gaggaactga tgtgcataat 11449
 gcatcaggct ggtacattag atccccgctt accgcgggca atatagcaac actaaaaact 11509
 cgatgtactt ccgaggaagc gcagtgcata atgctgcgca gtgttgccac ataaccacta 11569
 tattaaccat ttatctagcg gacgccaaaa actcaatgta tttctgagga agcgtggtgc 11629
 ataatgccac gcagcgtctg cataactttt attatttctt ttattaatca acaaaatttt 11689
 gtttttaaca tttc 11703

<210> 16
 <211> 64
 <212> PRT
 <213> Sindbis virus

<400> 16

Ser Ala Ala Pro Leu Val Thr Ala Met Cys Leu Leu Gly Asn Val Ser
 1 5 10 15

Phe Pro Cys Asp Arg Pro Pro Thr Cys Tyr Thr Arg Glu Pro Ser Arg
 20 25 30

Ala Leu Asp Ile Leu Glu Glu Asn Val Asn His Glu Ala Tyr Asp Thr
 35 40 45

Leu Leu Asn Ala Ile Leu Arg Cys Gly Ser Ser Gly Arg Ser Lys Arg
 50 55 60

<210> 17
 <211> 423
 <212> PRT
 <213> Sindbis virus

<400> 17

Ser Val Ile Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Thr Cys
 1 5 10 15

Ser Tyr Cys His His Thr Val Pro Cys Phe Ser Pro Val Lys Ile Glu
 20 25 30

Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser
 35 40 45

Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr
 50 55 60

Arg Tyr Met Ser Leu Lys Gln Asp His Thr Val Lys Glu Gly Thr Met
 65 70 75 80

Asp Asp Ile Lys Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr
 85 90 95

Lys Gly Tyr Phe Leu Leu Ala Lys Cys Pro Pro Gly Asp Ser Val Thr
 100 105 110

Val Ser Ile Val Ser Ser Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg
 115 120 125

Lys Ile Lys Pro Lys Phe Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro
 130 135 140

Val His Gly Lys Lys Ile Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu
 145 150 155 160

Thr Thr Ala Gly Tyr Ile Thr Met His Arg Pro Arg Pro His Ala Tyr
 165 170 175

Thr Ser Tyr Leu Glu Glu Ser Ser Gly Lys Val Tyr Ala Lys Pro Pro
 180 185 190

Ser Gly Lys Asn Ile Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Lys Thr
 195 200 205

Gly Thr Val Ser Thr Arg Thr Glu Ile Thr Gly Cys Thr Ala Ile Lys
 210 215 220

Gln Cys Val Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser
 225 230 235 240

Pro Asp Leu Ile Arg His Asp Asp His Thr Ala Gln Gly Lys Leu His
 245 250 255

Leu Pro Phe Lys Leu Ile Pro Ser Thr Cys Met Val Pro Val Ala His
 260 265 270

Ala Pro Asn Val Ile His Gly Phe Lys His Ile Ser Leu Gln Leu Asp

275 280 285
 Thr Asp His Leu Thr Leu Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro
 290 295 300
 Glu Pro Thr Thr Glu Trp Ile Val Gly Lys Thr Val Arg Asn Phe Thr
 305 310 315 320
 Val Asp Arg Asp Gly Leu Glu Tyr Ile Trp Gly Asn His Glu Pro Val
 325 330 335
 Arg Val Tyr Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro
 340 345 350
 His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile
 355 360 365
 Leu Ala Val Ala Ser Ala Thr Val Ala Met Met Ile Gly Val Thr Val
 370 375 380
 Ala Val Leu Cys Ala Cys Lys Ala Arg Arg Glu Cys Leu Thr Pro Tyr
 385 390 395 400
 Ala Leu Ala Pro Asn Ala Val Ile Pro Thr Ser Leu Ala Leu Leu Cys
 405 410 415
 Cys Val Arg Ser Ala Asn Ala
 420

<210> 18
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Linker

<220>
 <221> CDS
 <222> (1)..(51)

<400> 18
 aga tct ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga 48
 Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

tct
Ser

51

<210> 19
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 19

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser

<210> 20
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Linker

<220>
<221> CDS
<222> (1)..(45)

<400> 20
ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga tct 45
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 21
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 21

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 22

<211> 1050
 <212> DNA
 <213> Bluetongue virus 10

<220>
 <221> CDS
 <222> (1)..(1050)
 <223> VP7 gene

<400> 22
 atg gac act atc gcc gca aga gca ctc act gtg atg cga gca tgt gct 48
 Met Asp Thr Ile Ala Ala Arg Ala Leu Thr Val Met Arg Ala Cys Ala
 1 5 10 15
 acg ctt caa gag gca aga att gtg ttg gaa gcc aat gtg atg gaa att 96
 Thr Leu Gln Glu Ala Arg Ile Val Leu Glu Ala Asn Val Met Glu Ile
 20 25 30
 ttg ggg ata gct atc aat agg tac aat gga ctc act tta cga gga gtg 144
 Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val
 35 40 45
 acg atg cgc ccg acc tcg tta gca caa aga aat gag atg ttt ttt atg 192
 Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met
 50 55 60
 tgt ttg gat atg atg ctg tct gct gct ggg ata aat gtt gga ccg ata 240
 Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile
 65 70 75 80
 tcg cca gac tat act caa cat atg gct acg att ggt gta cta gca aca 288
 Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr
 85 90 95
 ccg gaa ata cct ttt aca acg gaa gcg gcg aat gaa ata gca cga gtg 336
 Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val
 100 105 110
 act ggg gag act tcg aca tgg ggg cca gcg cgt cag cct tat ggt ttc 384
 Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe
 115 120 125
 ttc ctt gaa act gag gaa acc ttc caa cca ggg agg tgg ttc atg cgc 432
 Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg
 130 135 140
 gcc gct caa gca gta act gca gta gtg tgc ggt ccg gat atg att caa 480
 Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln
 145 150 155 160
 gtg tca ctt aat gct gga gcg aga gga gat gta caa cag ata ttt cag 528
 Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln
 165 170 175
 ggt cgt aat gat ccc atg atg ata tat tta gtg tgg agg aga atc gaa 576
 Gly Arg Asn Asp Pro Met Met Ile Tyr Leu Val Trp Arg Arg Ile Glu

180						185						190						
aac	ttt	gcg	atg	gcg	caa	ggt	aat	tca	cag	caa	act	caa	gcg	ggt	gtg	624		
Asn	Phe	Ala	Met	Ala	Gln	Gly	Asn	Ser	Gln	Gln	Thr	Gln	Ala	Gly	Val			
195						200						205						
act	gtc	agt	gtt	ggt	gga	gtt	gac	atg	agg	gcg	gga	cgc	att	ata	gcg	672		
Thr	Val	Ser	Val	Gly	Gly	Val	Asp	Met	Arg	Ala	Gly	Arg	Ile	Ile	Ala			
210						215						220						
tgg	gat	gga	cag	gcc	gcg	ctg	cat	gtg	cat	aat	ccg	aca	caa	cag	aat	720		
Trp	Asp	Gly	Gln	Ala	Ala	Leu	His	Val	His	Asn	Pro	Thr	Gln	Gln	Asn			
225						230						235						240
gcg	atg	gtg	caa	ata	cag	gtt	gtg	ttc	tat	ata	tct	atg	gat	aaa	act	768		
Ala	Met	Val	Gln	Ile	Gln	Val	Val	Phe	Tyr	Ile	Ser	Met	Asp	Lys	Thr			
245						250						255						
tta	aac	cag	tac	ccc	gct	ttg	act	gct	gag	att	ttc	aat	gtt	tac	agc	816		
Leu	Asn	Gln	Tyr	Pro	Ala	Leu	Thr	Ala	Glu	Ile	Phe	Asn	Val	Tyr	Ser			
260						265						270						
ttc	agg	gac	cac	aca	tgg	cat	ggg	cta	aga	acg	gcg	ata	tta	aac	aga	864		
Phe	Arg	Asp	His	Thr	Trp	His	Gly	Leu	Arg	Thr	Ala	Ile	Leu	Asn	Arg			
275						280						285						
acc	aca	ctg	cca	aac	atg	ctg	cca	cca	atc	ttc	cca	cca	aat	gat	cga	912		
Thr	Thr	Leu	Pro	Asn	Met	Leu	Pro	Pro	Ile	Phe	Pro	Pro	Asn	Asp	Arg			
290						295						300						
gat	agc	atc	tta	act	ctt	cta	ctt	tta	tct	aca	ctt	gct	gat	gtt	tac	960		
Asp	Ser	Ile	Leu	Thr	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Ala	Asp	Val	Tyr			
305						310						315						320
act	gtt	tta	agg	cca	gag	ttt	gcg	att	cac	ggc	gta	aat	ccg	atg	cca	1008		
Thr	Val	Leu	Arg	Pro	Glu	Phe	Ala	Ile	His	Gly	Val	Asn	Pro	Met	Pro			
325						330						335						
ggg	ccg	ctc	aca	cgt	gct	att	gcg	cgc	gcc	gcc	tat	gtg	tag			1050		
Gly	Pro	Leu	Thr	Arg	Ala	Ile	Ala	Arg	Ala	Ala	Tyr	Val						
340						345												

<210> 23
 <211> 349
 <212> PRT
 <213> Bluetongue virus 10

<400> 23

Met	Asp	Thr	Ile	Ala	Ala	Arg	Ala	Leu	Thr	Val	Met	Arg	Ala	Cys	Ala
1				5					10					15	

Thr	Leu	Gln	Glu	Ala	Arg	Ile	Val	Leu	Glu	Ala	Asn	Val	Met	Glu	Ile
			20					25					30		

Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val
 35 40 45
 Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met
 50 55 60
 Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile
 65 70 75 80
 Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr
 85 90 95
 Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val
 100 105 110
 Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe
 115 120 125
 Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg
 130 135 140
 Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln
 145 150 155 160
 Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln
 165 170 175
 Gly Arg Asn Asp Pro Met Met Ile Tyr Leu Val Trp Arg Arg Ile Glu
 180 185 190
 Asn Phe Ala Met Ala Gln Gly Asn Ser Gln Gln Thr Gln Ala Gly Val
 195 200 205
 Thr Val Ser Val Gly Gly Val Asp Met Arg Ala Gly Arg Ile Ile Ala
 210 215 220
 Trp Asp Gly Gln Ala Ala Leu His Val His Asn Pro Thr Gln Gln Asn
 225 230 235 240
 Ala Met Val Gln Ile Gln Val Val Phe Tyr Ile Ser Met Asp Lys Thr
 245 250 255

Leu Asn Gln Tyr Pro Ala Leu Thr Ala Glu Ile Phe Asn Val Tyr Ser
 260 265 270

Phe Arg Asp His Thr Trp His Gly Leu Arg Thr Ala Ile Leu Asn Arg
 275 280 285

Thr Thr Leu Pro Asn Met Leu Pro Pro Ile Phe Pro Pro Asn Asp Arg
 290 295 300

Asp Ser Ile Leu Thr Leu Leu Leu Leu Ser Thr Leu Ala Asp Val Tyr
 305 310 315 320

Thr Val Leu Arg Pro Glu Phe Ala Ile His Gly Val Asn Pro Met Pro
 325 330 335

Gly Pro Leu Thr Arg Ala Ile Ala Arg Ala Ala Tyr Val
 340 345

<210> 24
 <211> 585
 <212> DNA
 <213> *Coccidioides immitis*

<220>
 <221> CDS
 <222> (1)..(585)
 <223> Ag2/PRA gene

<400> 24
 atg cag ttc tct cac gct ctc atc gct ctc gtc gct gcc ggc ctc gcc 48
 Met Gln Phe Ser His Ala Leu Ile Ala Leu Val Ala Ala Gly Leu Ala
 1 5 10 15
 agt gcc cag ctc cca gac atc cca cct tgc gct ctc aac tgc ttc gtt 96
 Ser Ala Gln Leu Pro Asp Ile Pro Pro Cys Ala Leu Asn Cys Phe Val
 20 25 30
 gag gct ctc ggc aac gat ggc tgc act cgc ttg acc gac ttc aag tgc 144
 Glu Ala Leu Gly Asn Asp Gly Cys Thr Arg Leu Thr Asp Phe Lys Cys
 35 40 45
 cac tgc tcc aag cct gag cta cca gga cag atc act cct tgc gtt gag 192
 His Cys Ser Lys Pro Glu Leu Pro Gly Gln Ile Thr Pro Cys Val Glu
 50 55 60
 gag gcc tgc cct ctc gac gcc cgt atc tcc gtc tcc aac atc gtc gtt 240
 Glu Ala Cys Pro Leu Asp Ala Arg Ile Ser Val Ser Asn Ile Val Val
 65 70 75 80
 gac cag tgc tcc aag gcc ggt gtc cca att gac atc cca cca gtt gac 288

Asp	Gln	Cys	Ser	Lys	Ala	Gly	Val	Pro	Ile	Asp	Ile	Pro	Pro	Val	Asp	
				85					90					95		
acc	acc	gcc	gct	ccc	gag	cca	tcc	gag	acc	gct	gag	ccc	acc	gct	gag	336
Thr	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Glu	Thr	Ala	Glu	Pro	Thr	Ala	Glu	
			100					105					110			
cca	acc	gag	gag	ccc	act	gcc	gag	cct	acc	gct	gag	ccc	acc	gct	gag	384
Pro	Thr	Glu	Glu	Pro	Thr	Ala	Glu	Pro	Thr	Ala	Glu	Pro	Thr	Ala	Glu	
		115					120					125				
ccg	act	cat	gag	ccc	acc	gag	gag	ccc	act	gcc	gtc	cca	acc	ggc	act	432
Pro	Thr	His	Glu	Pro	Thr	Glu	Glu	Pro	Thr	Ala	Val	Pro	Thr	Gly	Thr	
	130					135					140					
ggc	ggt	ggt	gtc	ccc	act	ggc	acc	ggt	tcc	ttc	acc	gtc	act	ggc	aga	480
Gly	Gly	Gly	Val	Pro	Thr	Gly	Thr	Gly	Ser	Phe	Thr	Val	Thr	Gly	Arg	
145					150				155						160	
cca	act	gcc	tcc	acc	cca	gct	gag	ttc	cca	ggt	gct	ggc	tcc	aac	gtc	528
Pro	Thr	Ala	Ser	Thr	Pro	Ala	Glu	Phe	Pro	Gly	Ala	Gly	Ser	Asn	Val	
				165				170						175		
cgt	gcc	agc	gtt	ggc	ggc	att	gct	gct	gct	ctc	ctc	ggt	ctc	gct	gcc	576
Arg	Ala	Ser	Val	Gly	Gly	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Leu	Ala	Ala	
			180				185						190			
tac	ctg	taa														585
Tyr	Leu															

<210> 25
 <211> 194
 <212> PRT
 <213> *Coccidioides immitis*

<400> 25

Met	Gln	Phe	Ser	His	Ala	Leu	Ile	Ala	Leu	Val	Ala	Ala	Gly	Leu	Ala	
1				5					10					15		
Ser	Ala	Gln	Leu	Pro	Asp	Ile	Pro	Pro	Cys	Ala	Leu	Asn	Cys	Phe	Val	
			20					25					30			
Glu	Ala	Leu	Gly	Asn	Asp	Gly	Cys	Thr	Arg	Leu	Thr	Asp	Phe	Lys	Cys	
		35					40					45				
His	Cys	Ser	Lys	Pro	Glu	Leu	Pro	Gly	Gln	Ile	Thr	Pro	Cys	Val	Glu	
	50					55					60					
Glu	Ala	Cys	Pro	Leu	Asp	Ala	Arg	Ile	Ser	Val	Ser	Asn	Ile	Val	Val	
65					70					75					80	

Asp Gln Cys Ser Lys Ala Gly Val Pro Ile Asp Ile Pro Pro Val Asp
85 90 95

Thr Thr Ala Ala Pro Glu Pro Ser Glu Thr Ala Glu Pro Thr Ala Glu
100 105 110

Pro Thr Glu Glu Pro Thr Ala Glu Pro Thr Ala Glu Pro Thr Ala Glu
115 120 125

Pro Thr His Glu Pro Thr Glu Glu Pro Thr Ala Val Pro Thr Gly Thr
130 135 140

Gly Gly Gly Val Pro Thr Gly Thr Gly Ser Phe Thr Val Thr Gly Arg
145 150 155 160

Pro Thr Ala Ser Thr Pro Ala Glu Phe Pro Gly Ala Gly Ser Asn Val
165 170 175

Arg Ala Ser Val Gly Gly Ile Ala Ala Ala Leu Leu Gly Leu Ala Ala
180 185 190

Tyr Leu

<210> 26
<211> 906
<212> DNA
<213> Streptococcus pneumoniae

<220>
<221> CDS
<222> (1)..(906)
<223> PspA gene

<400> 26
gaa gaa tct ccc gta gcc agt cag tct aaa gct gag aaa gac tat gat 48
Glu Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp
1 5 10 15

gca gcg aag aaa gat gct aag aat gcg aaa aaa gca gta gaa gat gct 96
Ala Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala
20 25 30

caa aag gct tta gat gat gca aaa gct gct cag aaa aaa tat gac gag 144
Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu
35 40 45

gat	cag	aag	aaa	act	gag	gag	aaa	gcc	gcg	cta	gaa	aaa	gca	gcg	tct	192
Asp	Gln	Lys	Lys	Thr	Glu	Glu	Lys	Ala	Ala	Leu	Glu	Lys	Ala	Ala	Ser	
50							55				60					
gaa	gag	atg	gat	aag	gca	gtg	gca	gca	ggt	caa	caa	gcg	tat	cta	gcc	240
Glu	Glu	Met	Asp	Lys	Ala	Val	Ala	Ala	Val	Gln	Gln	Ala	Tyr	Leu	Ala	
65					70					75					80	
tat	caa	caa	gct	aca	gac	aaa	gcc	gca	aaa	gac	gca	gca	gat	aag	atg	288
Tyr	Gln	Gln	Ala	Thr	Asp	Lys	Ala	Ala	Lys	Asp	Ala	Ala	Asp	Lys	Met	
				85					90					95		
ata	gat	gaa	gct	aag	aaa	cgc	gaa	gaa	gag	gca	aaa	act	aaa	ttt	aat	336
Ile	Asp	Glu	Ala	Lys	Lys	Arg	Glu	Glu	Glu	Ala	Lys	Thr	Lys	Phe	Asn	
			100					105					110			
act	ggt	cga	gca	atg	gta	ggt	cct	gag	cca	gag	cag	ttg	gct	gag	act	384
Thr	Val	Arg	Ala	Met	Val	Val	Pro	Glu	Pro	Glu	Gln	Leu	Ala	Glu	Thr	
			115				120					125				
aag	aaa	aaa	tca	gaa	gaa	gct	aaa	caa	aaa	gca	cca	gaa	ctt	act	aaa	432
Lys	Lys	Lys	Ser	Glu	Glu	Ala	Lys	Gln	Lys	Ala	Pro	Glu	Leu	Thr	Lys	
	130					135					140					
aaa	cta	gaa	gaa	gct	aaa	gca	aaa	tta	gaa	gag	gct	gag	aaa	aaa	gct	480
Lys	Leu	Glu	Glu	Ala	Lys	Ala	Lys	Leu	Glu	Glu	Ala	Glu	Lys	Lys	Ala	
145					150					155					160	
act	gaa	gcc	aaa	caa	aaa	gtg	gat	gct	gaa	gaa	gtc	gct	cct	caa	gct	528
Thr	Glu	Ala	Lys	Gln	Lys	Val	Asp	Ala	Glu	Glu	Val	Ala	Pro	Gln	Ala	
				165				170						175		
aaa	atc	gct	gaa	ttg	gaa	aat	caa	ggt	cat	aga	cta	gaa	caa	gag	ctc	576
Lys	Ile	Ala	Glu	Leu	Glu	Asn	Gln	Val	His	Arg	Leu	Glu	Gln	Glu	Leu	
			180					185					190			
aaa	gag	att	gat	gag	tct	gaa	tca	gaa	gat	tat	gct	aaa	gaa	ggt	ttc	624
Lys	Glu	Ile	Asp	Glu	Ser	Glu	Ser	Glu	Asp	Tyr	Ala	Lys	Glu	Gly	Phe	
		195					200					205				
cgt	gct	cct	ctt	caa	tct	aaa	ttg	gat	gcc	aaa	aaa	gct	aaa	cta	tca	672
Arg	Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Ala	Lys	Lys	Ala	Lys	Leu	Ser	
	210					215						220				
aaa	ctt	gaa	gag	tta	agt	gat	aag	att	gat	gag	tta	gac	gct	gaa	att	720
Lys	Leu	Glu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	Glu	Ile	
225					230					235					240	
gca	aaa	ctt	gaa	gat	caa	ctt	aaa	gct	gct	gaa	gaa	aac	aat	aat	gta	768
Ala	Lys	Leu	Glu	Asp	Gln	Leu	Lys	Ala	Ala	Glu	Glu	Asn	Asn	Asn	Val	
				245				250						255		
gaa	gac	tac	ttt	aaa	gaa	ggt	tta	gag	aaa	act	att	gct	gct	aaa	aaa	816
Glu	Asp	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Ile	Ala	Ala	Lys	Lys	
			260					265					270			

gct gaa tta gaa aaa act gaa gct gac ctt aag aaa gca gtt aat gag 864
 Ala Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu
 275 280 285

cca gaa aaa cca gct cca gct cca gaa act cca gcc cca gaa 906
 Pro Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu
 290 295 300

<210> 27

<211> 302

<212> PRT

<213> Streptococcus pneumoniae

<400> 27

Glu Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp
 1 5 10 15

Ala Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala
 20 25 30

Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu
 35 40 45

Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser
 50 55 60

Glu Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala
 65 70 75 80

Tyr Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met
 85 90 95

Ile Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn
 100 105 110

Thr Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr
 115 120 125

Lys Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys
 130 135 140

Lys Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala
 145 150 155 160

Thr Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala

165	170	175
Lys Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu 180 185 190		
Lys Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe 195 200 205		
Arg Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser 210 215 220		
Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile 225 230 235 240		
Ala Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val 245 250 255		
Glu Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys 260 265 270		
Ala Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu 275 280 285		
Pro Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu 290 295 300		